SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> MODIFIED ANTIBODY AGAINST CD22 AND UTILIZATION THEREOF

<130> C1-A0305P

<150> JP 2003-96950

<151> 2003-03-31

<160> 36

<170> PatentIn version 3.1

<210> 1

<211> 260

<212> PRT

<213> Artificial

<220>

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Met Glu Arg His Trp Ile Phe Leu Phe Leu Phe Ser Val Thr Ala Gly

1 5 10 15

Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Tyr Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn
65 70 75 80

Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly
115 120 125

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Asn Val Thr

145 150 155 160

Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ala Asn His Lys
165 170 175

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
180 185 190

Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
195 200 205

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Val
210 215 220

Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln Tyr Leu Ser Ser
225 230 235 240

Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp
245 250 255

Asp Asp Asp Lys
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<210> 2

<211> 810

<212> DNA

<213> Artificial

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<221> CDS

<222> (14)..(799)

<223>

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gta act gca ggt gtc cac tcc cag gtc cag ctg cag gag tca ggg gct 97
Val Thr Ala Gly Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Ala
15 20 25

gaa ctg tca aaa cct ggg gcc tca gtg aag atg tcc tgc aag gct tct 145
Glu Leu Ser Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser
30 35 40

ggc tac acc ttt act agc tac tgg ctg cac tgg ata aaa cag agg cct 193
Gly Tyr Thr Phe Thr Ser Tyr Trp Leu His Trp Ile Lys Gln Arg Pro

45 50 55 60

gga cag ggt ctg gaa tgg att gga tac att aat cct agg aat gat tat 241
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn Asp Tyr
65 70 75

act gag tac aat cag aac ttc aag gac aag gcc aca ttg act gca gac 289
Thr Glu Tyr Asn Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp
80 85 90

aaa tcc tcc agc aca gcc tac atg caa ctg agc agc ctg aca tct gag 337
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
95 100 105

gac tct gca gtc tat tac tgt gca aga agg gat att act acg ttc tac 385
Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr Phe Tyr
110 115 120

tgg ggc caa ggc acc act ctc aca gtc tcc tcg ggt gga ggc ggt agc 433
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser
125 130 135 140

gac att cag ctg acc cag tct cca tca tct ctg gct gtg tct gca gga 481
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
145 150 155

gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 529
Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
160 165 170

gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 577
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
175 180 185

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 625
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
190 195 200

cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 673
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
205 210 215 220

atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 721
Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
225 230 235

tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 769
Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
240 245 250

gac tac aag gat gac gac gat aag tga taa gcggccgcaa t 810
Asp Tyr Lys Asp Asp Asp Asp Lys

255 260

<210> 3

<211> 262

<212> PRT

<213> Artificial

<220>

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Val Lys Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe
35 40 45

Ser Ile Tyr Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro
65 70 75 80

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu
115 120 125

Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly
130 135 140

Gly Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala
145 150 155 160

Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile
165 170 175

Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys
180 185 190

Leu Leu Ile Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Lys
195 200 205

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn

210 215 220

Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr
225 230 235 240

Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr
245 250 255

Lys Asp Asp Asp Asp Lys
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<210> 4
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<213> Artificial

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<221> CDS
<222> (14)..(805)
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                1               5                   10

act tta aaa ggt gtg aag tgt gaa gtg cag ctg gtg gag tct ggg gga      97
Thr Leu Lys Gly Val Lys Cys Glu Val Gln Leu Val Glu Ser Gly Gly
        15                  20                  25

ggc tta gtg aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct     145
Gly Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
    30                  35                  40

gga ttc gct ttc agt atc tat gac atg tct tgg gtt cgc cag act ccg     193
Gly Phe Ala Phe Ser Ile Tyr Asp Met Ser Trp Val Arg Gln Thr Pro
45                  50                  55                  60

gag aag agg ctg gag tgg gtc gca tac att agt agt ggt ggt ggt acc     241
Glu Lys Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Gly Thr
                65                  70                  75

acc tac tat cca gac act gtg aag ggc cga ttc acc atc tcc aga gac     289
Thr Tyr Tyr Pro Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
            80                  85                  90

aat gcc aag aac acc ctg tac ctg caa atg agc agt ctg aag tct gag     337
Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu
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95 100 105

gac aca gcc atg tat tac tgt gca aga cat agt ggc tac ggt agt agc 385
Asp Thr Ala Met Tyr Tyr Cys Ala Arg His Ser Gly Tyr Gly Ser Ser
110 115 120

tac ggg gtt ttg ttt gct tac tgg ggc caa ggg act ctg gtc act gtc 433
Tyr Gly Val Leu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
125 130 135 140

tct gca ggt gga ggc ggt agc gat atc cag atg acc cag act aca tcc 481
Ser Ala Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser
145 150 155

tcc ctg tct gcc tct ctg gga gac aga gtc acc att agt tgc agg gca 529
Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
160 165 170

agt cag gac att agc aat tat tta aac tgg tat cag cag aaa cca gat 577
Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
175 180 185

gga act gtt aaa ctc ctg atc tac tac aca tca ata tta cac tca gga 625
Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Ile Leu His Ser Gly
190 195 200

gtc cca tca aag ttc agt ggc agt ggg tct gga aca gat tat tct ctc 673
Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
205 210 215 220

acc att agc aac ctg gag caa gaa gat ttt gcc act tac ttt tgc caa 721
Thr Ile Ser Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln
225 230 235

cag ggt aat acg ctt ccg tgg acg ttc ggt gga ggc acc aag ctg gaa 769
Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
240 245 250

atc aaa gac tac aag gat gac gac gat aag tga taa gcggccgcaa t 816
Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys
255 260

<210> 5
<211> 116
<212> PRT
<213> Artificial

<220>
<223> an artificially synthesized peptide sequence

<400> 5

Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
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<210> 6

<211> 348

<212> DNA

<213> Artificial

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<221> CDS

<222> (1)..(348)

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1 5 10 15

tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att 144
Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac 240
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt 288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc 336
Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

aca gtc tcc tcg 348
Thr Val Ser Ser
115

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<211> 112
<212> PRT
<213> Artificial

<220>

<223> an artificially synthesized peptide sequence

<400> 7

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
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Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 8

<211> 336

<212> DNA

<213> Artificial

<220>

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<220>

<221> CDS

<222> (1)..(336)

<223>

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Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288
Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
85 90 95

tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336
Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 9
<211> 123
<212> PRT
<213> Artificial

<220>
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<400> 9

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
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Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
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<210> 10

<211> 369

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<222> (1)..(369)

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tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc gct ttc agt atc tat      96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
            20                  25                  30

gac atg tct tgg gtt cgc cag act ccg gag aag agg ctg gag tgg gtc     144
Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35                  40                  45

gca tac att agt agt ggt ggt ggt acc acc tac tat cca gac act gtg     192
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Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc ctg tac 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg agc agt ctg aag tct gag gac aca gcc atg tat tac tgt 288
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

gca aga cat agt ggc tac ggt agt agc tac ggg gtt ttg ttt gct tac 336
Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

tgg ggc caa ggg act ctg gtc act gtc tct gca 369
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

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<211> 107

<212> PRT

<213> Artificial

<220>

<223> an artificially synthesized peptide sequence

<400> 11

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Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 12

<211> 321

<212> DNA

<213> Artificial

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<221> CDS

<222> (1)..(321)

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Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gac aga gtc acc att agt tgc agg gca agt cag gac att agc aat tat 96
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

tta aac tgg tat cag cag aaa cca gat gga act gtt aaa ctc ctg atc 144
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

tac tac aca tca ata tta cac tca gga gtc cca tca aag ttc agt ggc 192

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly
50 55 60

agt ggg tct gga aca gat tat tct ctc acc att agc aac ctg gag caa 240
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

gaa gat ttt gcc act tac ttt tgc caa cag ggt aat acg ctt ccg tgg 288
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

acg ttc ggt gga ggc acc aag ctg gaa atc aaa 321
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 13
<211> 88
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized DNA sequence

<400> 13
cctgaattcc accatggaaa ggcactggat ctttctcttc ctgttttcag taactgcagg 60

tgtccactcc caggtccagc tgcaggag 88

<210> 14

<211> 90

<212> DNA

<213> Artificial

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<223> an artificially synthesized DNA sequence

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gaggcctgga cagggtctgg aatggattgg 90

<210> 15

<211> 87

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 15

cttcaaggac aaggccacat tgactgcaga caaatcctcc agcacagcct acatgcaact 60

gagcagcctg acatctgagg actctgc 87

<210> 16

<211> 88

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 16

ggcaccactc tcacagtctc ctcgggtgga ggcggtagcg acattcagct gacccagtct 60

ccatcatctc tggctgtgtc tgcaggag 88

<210> 17

<211> 91

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 17

cagtgcaaat cacaagaact acttggcctg gtaccagcag aaaccagggc agtctcctaa 60

actgctgatc tactgggcat ccactaggga a 91

<210> 18

<211> 105

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 18

ggcagcggat ctgggacaga ttttactctt accatcagca gagtacaagt tgaagacctg 60

gcaatttatt attgtcacca atacctctcc tcgtggacgt tcggt 105

<210> 19

<211> 91

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 19

ggtgtagcca gaagccttgc aggacatctt cactgaggcc ccaggttttg acagttcagc 60

ccctgactcc tgcagctgga cctgggagtg g 91

<210> 20

<211> 96

<212> DNA

<213> Artificial

<220>

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<400> 20

tgcagtcaat gtggccttgt ccttgaagtt ctgattgtac tcagtataat cattcctagg 60

attaatgtat ccaatccatt ccagaccctg tccagg 96

<210> 21

<211> 105

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 21

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tgcacagtaa tagactgcag agtcctcaga tgtcaggctg ctcag 105

<210> 22

<211> 102

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 22

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catagtgacg ttttctcctg cagacacagc cagagatgat gg 102

<210> 23

<211> 84

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 23

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agtggatgcc cagtagatca gcag 84

<210> 24

<211> 93

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 24

attgcggccg cttatcactt atcgtcgtca tccttgtagt ctttgatctc cagcttggtc 60

cctccaccga acgtccacga ggagaggtat tgg 93

<210> 25

<211> 92

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 25

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tgtgaagtgt gaagtgcagc tggtggagtc tg 92

<210> 26

<211> 89

<212> DNA

<213> Artificial

<220>

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<400> 26

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agaagaggct ggagtgggtc gcatacatt 89

<210> 27

<211> 86

<212> DNA

<213> Artificial

<220>

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<400> 27

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tctgaagtct gaggacacag ccatgt 86

<210> 28

<211> 98

<212> DNA

<213> Artificial

<220>

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<400> 28

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cggtagcgat atccagatga cccagactac atcctccc 98

<210> 29

<211> 114

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 29

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aactgttaaa ctcctgatct actacacatc aatattacac tcaggagtcc catc 114

<210> 30

<211> 87

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 30

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atacgcttcc gtggacgttc ggtggag 87

<210> 31

<211> 91

<212> DNA

<213> Artificial

<220>

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<400> 31

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cctcccccag actccaccag ctgcacttca c 91

<210> 32

<211> 91

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 32

gtctctggag atggtgaatc ggcccttcac agtgtctgga tagtaggtgg taccaccacc 60

actactaatg tatgcgaccc actccagcct c 91

<210> 33

<211> 90

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

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aatacatggc tgtgtcctca gacttcagac 90

<210> 34

<211> 90

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 34

taattgctaa tgtcctgact tgccctgcaa ctaatggtga ctctgtctcc cagagaggca 60

gacagggagg atgtagtctg ggtcatctgg 90

<210> 35

<211> 93

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

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tttgatggga ctcctgagtg taatattgat gtg 93

<210> 36

<211> 85

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized DNA sequence

<400> 36

attgcggccg cttatcactt atcgtcgtca tccttgtagt ctttgatttc agcttggtg 60

cctccaccga acgtccacgg aagcg 85